



NCBI

NCBI Conserved Domain Summary

PubMed

Nucleotide

Protein

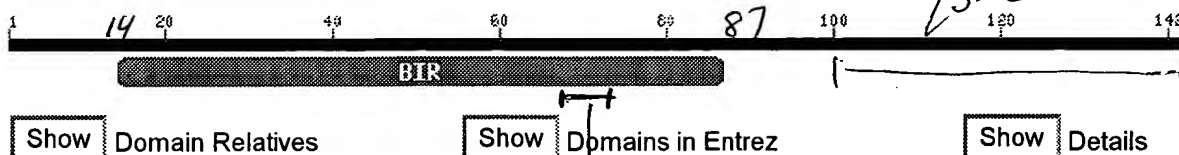
Structure

Taxonomy

Query= gi|2315863|gb|AAC51660.1| apoptosis inhibitor survivin
[Homo sapiens]
(142 letters)

Database: cdd.v.1.62

Click on boxes for multiple alignments



SEQ ID NO:3
fusion
for Ab

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SEQ ID NO:4, essential
residues 65-74 of SEQ ID NO:3

BIR: Baculovirus Inhibition of apoptosis Regulator



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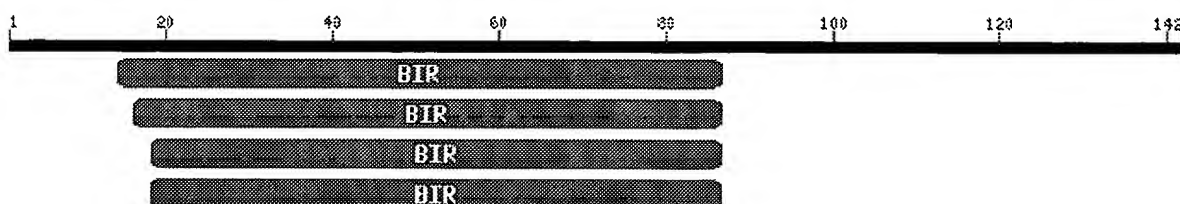
Taxonomy

RPS-BLAST 2.2.6 [Apr-09-2003]

Query= gi|2315863|gb|AAC51660.1| apoptosis inhibitor survivin
[Homo sapiens]
(142 letters)

Database: #cdd.v1.62
11,088 PSSMs; 2,717,223 total columns

Click on boxes for multiple alignments



Show Domain Relatives

- .. This CD alignment includes 3D structure. To display structure, download [Cn3D!](#)

PSSMs producing significant alignments:

Score E
(bits) value

- [gnl|CDD|14931](#) smart00238, BIR, Baculoviral inhibition of apoptosis protein r... [89.6](#) 1e-19
- [gnl|CDD|17763](#) cd00022, BIR, Baculoviral inhibition of apoptosis protein repe... [84.2](#) 5e-18
- [gnl|CDD|3661](#) LOAD_bir, BIR, Zn binding domain involved in protein protein i... [79.2](#) 2e-16
- [gnl|CDD|1211](#) pfam00653, BIR, Inhibitor of Apoptosis domain. BIR stands for ... [78.4](#) 3e-16

- [gnl|CDD|14931](#), smart00238, BIR, Baculoviral inhibition of apoptosis protein repeat; Domain found in inhibitor of apoptosis proteins (IAPs) and other proteins. Acts as a direct inhibitor of caspase enzymes.

CD-Length = 72 residues, 95.8% aligned
Score = 89.6 bits (222), Expect = 1e-19

```
Query: 14 LKDHRISTFKNWPFLGCACTPERMAEAGFIHCPTENEPDLAQCFFCFKELEGWEPDDDDP 73
Sbjct: 2 SEEARLKTFFQNPYNS--KLTPEKLAKAGFYTGTV---GDEVKCFFCGGELDNWEPGDDP 56

Query: 74 IEEHKKHSSGCAFL 87
Sbjct: 57 WEEHKKWSPNCPFV 70
```

- [gnl|CDD|17763](#), cd00022, BIR, Baculoviral inhibition of apoptosis protein repeat domain; Found in inhibitors of apoptosis proteins (IAPs) and other proteins. In higher eukaryotes, BIR domains inhibit apoptosis by acting as direct inhibitors of the caspase family of protease enzymes. In yeast, BIR domains are involved in regulating cytokinesis. This novel fold is stabilized by zinc tetrahedrally coordinated by one histidine and three cysteine residues and resembles a classical zinc finger.

CD-Length = 69 residues, 97.1% aligned
Score = 84.2 bits (208), Expect = 5e-18

```
Query: 16 DHRISTFKNWPFLGCACTPERMAEAGFIHCPTENEPDLAQCFKFCFKELEGWEPDDDDPIE 75
Sbjct: 1 EARLKTFKNWPI--SLKVTPEKLAEAGFYTT---GRGDEVKCFKFCGLELKNWEPGDDPW 55

Query: 76 EHKHSSGCAFL 87
Sbjct: 56 EHKRWSPNCPFV 67
```

- [gnl|CDD|3661](#), LOAD_bir, BIR, Zn binding domain involved in protein protein interactions in caspase inhibition and spindle assembly.

CD-Length = 65 residues, 100.0% aligned
Score = 79.2 bits (195), Expect = 2e-16

```
Query: 18 RISTFKNWPFLGCACTPERMAEAGFIHCPTENEPDLAQCFKFCFKELEGWEPDDDDPIEEH 77
Sbjct: 1 RLKTFQNWPA--SLNVLPEKLARAGFYTTGR---GDEVRCFFCGGVLKNWEPGDDPWEEH 55

Query: 78 KKHSSGCAFL 87
Sbjct: 56 ARWSPNCPFV 65
```

[gnl|CDD|1211](#), pfam00653, BIR, Inhibitor of Apoptosis domain. BIR stands for 'Baculovirus Inhibitor of apoptosis protein Repeat' Also known as IAP repeat.

CD-Length = 66 residues, 98.5% aligned
Score = 78.4 bits (193), Expect = 3e-16

```
Query: 18 RISTFKNWPFLGCACTPERMAEAGFIHCPTENEPDLAQCFKFCFKELEGWEPDDDDPIEEH 77
Sbjct: 1 RLRTFQNWPI--SNLQFPEQLAKAGFYTTGVGDEV---RCFFCGVELKNWEPGDDPWEEH 55

Query: 78 KKHSSGCAFL 87
Sbjct: 56 KRWSPNCPFV 65
```

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